

SEQUENCE LISTING

<110> Duke University
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<120> GENERATION OF RECOMBINANT ADENO-ASSOCIATED VIRAL VECTORS BY A
COMPLETE ADENOVIRUS-MEDIATED APPROACH

<130> 180/137

<150> US 60/349,532

<151> 2002-01-18

<160> 22

<170> PatentIn version 3.2

<210> 1

<211> 1611

<212> DNA

<213> adeno-associated virus 2

<220>

<221> CDS

<222> (1)..(1611)

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Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu	
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile	
35 40 45	
gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg	192
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu	
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acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg	240
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val	
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caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa	288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu	
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acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att	336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	
100 105 110	
cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg	384
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu	
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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly	
130 135 140	
aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aaa	480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys	
145 150 155 160	

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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His	
180 185 190	
ctg acg cac gtg tcg cag acg cag gag cag aac aaa gag aat cag aat	624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn	
195 200 205	
ccc aat tct gat gcg ccg gtg atc aga tca aaa act tca gcc agg tac	672
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Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
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att atg agc ctg act aaa acc gcc ccc gac tac ctg gtg ggc cag cag	864
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala	
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Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg	
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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val	
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atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac tca	1296
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser	
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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe	
435 440 445	
gaa ctc acc cgc cgt ctg gat cat gac ttt ggg aag gtc acc aag cag	1392
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln	
450 455 460	
gaa gtc aaa gac ttt ttc cgg tgg gca aag gat cac gtg gtt gag gtg	1440
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val	
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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala	
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ccc agt gac gca gat ata agt gag ccc aaa cgg gtg cgc gag tca gtt	1536
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val	
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gcg cag cca tcg acg tca gac gcg gaa gct tcg atc aac tac gca gac	1584
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp	
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Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val	
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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu	
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Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	
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Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu	
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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
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Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
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Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 370 375 380

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Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att 144
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
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Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
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Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80

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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu	
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acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att	336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	
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cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg	384
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu	
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Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly	
130 135 140	
aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aag	480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys	
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165 170 175	
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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His	
180 185 190	
ctg acg cac gtg tcg cag acg cag gag cag aac aaa gag aat cag aat	624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn	
195 200 205	
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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr	
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225 230 235 240	
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
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tcc aac tcg cgg tcc caa atc aag gct gcc ttg gac aat gcg gga aag	816
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
260 265 270	
att atg agc ctg act aaa acc gcc ccc gac tac ctg gtg ggc cag cag	864
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
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Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
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Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala	
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gaa gtc aaa gac ttt ttc cgg tgg gca aag gat cac gtg gtt gag gtg Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val 465 470 475 480	1440
gag cat gag ttc tac gtc aaa aag ggt gga gcc aag aaa aga ccc gcc Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala 485 490 495	1488
ccc agt gac gca gat ata agt gag ccc aaa cgg gtg cgc gag tca gtt Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val 500 505 510	1536
gcg cag cca tcg acg tca gac gcg gaa gct tcg atc aac tac gca gat Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp 515 520 525	1584
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Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
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Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
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Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
 100 105 110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
 115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
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Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
 145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
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Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
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Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
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 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
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 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
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 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
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 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
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 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
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 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
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 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
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Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
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Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
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gaactaatac	gatgggtaca	ggcagtggcg	caccaatggc	agacaataac	gagggcgccg	1980
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tcataccac	cagcaccgga	acctgggccc	tgcccaccta	caacaaccac	ctctacaaac	2100
aaatttccag	ccaatcagga	gcctcgaacg	acaatcacta	ctttgggtac	agcaccctt	2160
gggggtat	tgacttcaac	agattccact	gccacttttc	accacgtgac	tggcaaagac	2220
tcatacaaa	caactgggga	ttccgaccca	agagactcaa	cttcaagctc	tttaacattc	2280
aagtcaaaga	ggtcacgcag	aatgacggta	cgacgacgat	tgccaataac	cttaccagca	2340
cgggttcagg	gtttactgac	tcggagtacc	agctcccgtg	cgctcctcgg	tcggcgcatc	2400
aaggatgcct	cccgcggttc	ccagcagacg	tcttcatggg	gccacagtat	ggatacctca	2460
ccctgaacaa	cgggagtcag	gcagtaggac	gctcttcatt	ttactgcctg	gagtactttc	2520
cttctcagat	gctgcgtacc	ggaaacaact	ttaccttcag	ctacactttt	gaggacgttc	2580
ctttccacag	cagctacgct	cacagccaga	gtctggaccg	tctcatgaat	cctctcatcg	2640
accagtacct	gtattacttg	agcagaacaa	acactccaag	tggaaccacc	acgcagtcaa	2700
ggcttcagtt	ttctcaggcc	ggagcgagtg	acattcggga	ccagtctagg	aactggcttc	2760
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aatactcgtg	gactggagct	accaagtacc	acctcaatgg	cagagactct	ctggtgaatc	2880
cgggcccgcc	catggcaagc	cacaaggacg	atgaagaaaa	gttttttctc	cagagcgggg	2940
ttctcatctt	tgggaagcaa	ggctcagaga	aaacaaatgt	ggacattgaa	aaggtcatga	3000
ttacagacga	agaggaaatc	aggacaacca	atcccgtggc	tacggagcag	tatggttctg	3060

tatctacca cctccagaga ggcaacagac aagcagctac cgcagatgtc aacacacaag 3120
 gcgtttcttc aggcattgtc tggcaggaca gagatgtgta ccttcagggg cccattctggg 3180
 caaagattcc acacacggac ggacattttc acccctctcc cctcatgggt ggattcggac 3240
 ttaaacaccc tctccacag attctcatca agaacacccc ggtacctgcy aatccttcga 3300
 ccaccttcag tgcggcaaag ttgcttcct tcatcacaca gtactccacg ggacagggtca 3360
 gcgtggagat cgagtgggag ctgcagaagg aaaacagcaa acgctggaat cccgaaattc 3420
 agtacacttc caactacaac aagtctgtta atgtggactt tactgtggac actaatggcg 3480
 tgtattcaga gcctcgcccc attggcacca gatacctgac tcgtaatctg taattgcttg 3540
 ttaatcaata aaccgtttta ttcgtttcag ttga 3574

<210> 6
 <211> 312
 <212> PRT
 <213> adeno-associated virus 2

<400> 6

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1 5 10 15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35 40 45

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50 55 60

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65 70 75 80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85 90 95

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210 215 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300

Arg Leu Ala Arg Gly His Ser Leu
305 310

<210> 7
<211> 397
<212> PRT
<213> adeno-associated virus 2

<400> 7

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1 5 10 15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50 55 60

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 210 215 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 225 230 235 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 245 250 255

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
 260 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 275 280 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290 295 300

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
 305 310 315 320

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
 325 330 335

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
 340 345 350

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
 355 360 365

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
 370 375 380

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 385 390 395

<210> 8
 <211> 2478
 <212> DNA
 <213> adeno-associated virus 2

<400> 8
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 agagaatgaa tcagaattca aatatctgct tcactcacgg acagaaagac tgttttagagt 180
 gctttcccgt gtcagaatct caaccggtt ctgtcgtaa aaaggcgat cagaaactgt 240
 gctacattca tcatatcatg ggaaagggtgc cagacgcttg cactgcctgc gatctggtca 300
 atgtggattt ggatgactgc atctttgaac aataaatgat ttaaatacagg tatggctgcc 360
 gatggttatc ttccagattg gctcgaggac actctctctg aaggaataag acagtgggtg 420
 aagctcaaac ctggcccacc accaccaaag cccgcagagc ggcataagga cgacagcagg 480
 ggtcttgtgc ttctgggta caagtacctc ggacccttca acggactcga caaggagag 540
 ccggtcaacg aggcagacgc cgcggccctc gagcacgaca aagcctacga ccggcagctc 600
 gacagcggag acaaccgta cctcaagtac aaccacgccg acgcggagtt tcaggagcgc 660
 cttaaagaag atacgtcttt tgggggcaac ctcgagcagc cagtcttcca ggcgaaaaag 720
 agggttcttg aacctctggg cctggttgag gaacctgtta agacggctcc gggaaaaaag 780
 aggccggtag agcactctcc tgtggagcca gactcctcct cgggaaccgg aaaggcgggc 840
 cagcagcctg caagaaaaag attgaatttt ggtcagactg gagacgcaga ctacgtacct 900
 gacccccagc ctctcggaac gccaccagca gcccctctg gtctgggaac taatacgatg 960
 gctacaggca gtggcgacac aatggcagac aataacgagg gcgccgacgg agtgggtaat 1020
 tcctcgggaa attggcattg cgattccaca tggatgggag acagagtcac caccaccagc 1080
 acccgaacct gggccctgcc cacctacaac aaccacctc acaacaaat ttccagccaa 1140
 tcaggagcct cgaacgacaa tcaactctt ggctacagca ccccttgggg gtattttgac 1200
 ttcaacagat tccactgcca cttttacca cgtgactggc aaagactcat caacaacaac 1260
 tggggattcc gacccaagag actcaacttc aagctcttta acattcaagt caaagagggtc 1320
 acgcagaatg acggtacgac gacgattgcc aataacctta ccagcacggt tcagggtgttt 1380
 actgactcgg agtaccagct cccgtacgtc ctcggtcggc cgcatacagg atgcctcccg 1440
 ccgttcccag cagacgtctt catggtgcc cagtatggat acctcaccct gaacaacggg 1500
 agtcaggcag taggacgctc ttcatcttac tgcttgaggt actttccttc tcagatgctg 1560
 cgtaccgga acaactttac cttcagctac acttttgagg acgttccttt ccacagcagc 1620

tacgctcaca gccagagtct ggaccgtctc atgaatcctc tcatcgacca gtacctgtat 1680
 tacttgagca gaacaaacac tccaagtgga accaccacgc agtcaaggct tcagttttct 1740
 caggccggag cgagtgacat tcgggaccag tctaggaact ggcttcctgg accctgttac 1800
 cgccagcagc gagtatcaaa gacatctgcg gataacaaca acagtgaata ctctgtggact 1860
 ggagctacca agtaccacct caatggcaga gactctctgg tgaatccggg cccggccatg 1920
 gcaagccaca aggacgatga agaaaagttt tttcctcaga gcgggggttct catctttggg 1980
 aagcaaggct cagagaaaaac aaatgtggac attgaaaagg tcatgattac agacgaagag 2040
 gaaatcagga caaccaatcc cgtggctacg gagcagtatg gttctgtatc taccaacctc 2100
 cagagaggca acagacaagc agctaccgca gatgtcaaca cacaaggcgt tcttccaggc 2160
 atggtctggc aggacagaga tgtgtacctt cagggggccca tctgggcaaa gattccacac 2220
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 ccacagattc tcatcaagaa caccocggta cctgcgaatc cttcgaccac cttcagtgcg 2340
 gcaaagtttg cttccttcat cacacagtac tccacgggac aggtcagcgt ggagatcgag 2400
 tgggagctgc agaaggaaaa cagcaaacgc tggaatcccg aaattcagta cacttccaac 2460
 tacaacaagt ctgttaat 2478

<210> 9
 <211> 735
 <212> PRT
 <213> adeno-associated virus 2

<400> 9

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
 1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
 50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
 85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
 515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
 530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
 545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
 565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
 580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
 595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
 610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
 625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
 645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
 660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 10
<211> 598
<212> PRT
<213> adeno-associated virus 2
<400> 10

Met Ala Pro Gly Lys Lys Arg Pro Val Glu His Ser Pro Val Glu Pro
1 5 10 15

Asp Ser Ser Ser Gly Thr Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys
20 25 30

Arg Leu Asn Phe Gly Gln Thr Gly Asp Ala Asp Ser Val Pro Asp Pro
35 40 45

Gln Pro Leu Gly Gln Pro Pro Ala Ala Pro Ser Gly Leu Gly Thr Asn
50 55 60

Thr Met Ala Thr Gly Ser Gly Ala Pro Met Ala Asp Asn Asn Glu Gly
65 70 75 80

Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr
85 90 95

Trp Met Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu
100 105 110

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly
115 120 125

Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
130 135 140

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
145 150 155 160

Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe
165 170 175

Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Gln Asn Asp Gly Thr
 180 185 190
 Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
 195 200 205
 Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys
 210 215 220
 Leu Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
 225 230 235 240
 Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr
 245 250 255
 Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe
 260 265 270
 Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala
 275 280 285
 His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr
 290 295 300
 Leu Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln
 305 310 315 320
 Ser Arg Leu Gln Phe Ser Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln
 325 330 335
 Ser Arg Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser
 340 345 350
 Lys Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala
 355 360 365
 Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro
 370 375 380
 Ala Met Ala Ser His Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser
 385 390 395 400
 Gly Val Leu Ile Phe Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp
 405 410 415
 Ile Glu Lys Val Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn
 420 425 430
 Pro Val Ala Thr Glu Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg
 435 440 445

Gly Asn Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu
 450 455 460

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile
 465 470 475 480

Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
 485 490 495

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys
 500 505 510

Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys
 515 520 525

Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu
 530 535 540

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
 545 550 555 560

Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr
 565 570 575

Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg
 580 585 590

Tyr Leu Thr Arg Asn Leu
 595

<210> 11
 <211> 533
 <212> PRT
 <213> adeno-associated virus 2
 <400> 11

Met Ala Thr Gly Ser Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala
 1 5 10 15

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp
 20 25 30

Met Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro
 35 40 45

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala
 50 55 60

Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe
 65 70 75 80

Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
 85 90 95

Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys
 100 105 110

Leu Phe Asn Ile Gln Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr
 115 120 125

Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser
 130 135 140

Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu
 145 150 155 160

Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu
 165 170 175

Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys
 180 185 190

Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr
 195 200 205

Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His
 210 215 220

Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu
 225 230 235 240

Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser
 245 250 255

Arg Leu Gln Phe Ser Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser
 260 265 270

Arg Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys
 275 280 285

Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr
 290 295 300

Lys Tyr His Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala
 305 310 315 320

Met Ala Ser His Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly
 325 330 335

Val Leu Ile Phe Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile
 340 345 350

Glu Lys Val Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro
 355 360 365

Val Ala Thr Glu Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly
 370 375 380

Asn Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro
 385 390 395 400

Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
 405 410 415

Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met
 420 425 430

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn
 435 440 445

Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe
 450 455 460

Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile
 465 470 475 480

Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
 485 490 495

Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val
 500 505 510

Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr
 515 520 525

Leu Thr Arg Asn Leu
 530

<210> 12
 <211> 145
 <212> DNA
 <213> adeno-associated virus 2

<400> 12
 ttggccactc cctctctgcg cgctcgctcg ctactgagg ccgggcgacc aaaggtcgcc 60
 cgacgcccg gctttgccg ggcggcctca gtgagcgagc gagcgcgag agagggagtg 120
 gccaaactcca tctactagggg ttcct 145

<210> 13
 <211> 144
 <212> DNA
 <213> adeno-associated virus 2

<400> 13
 ggaacccta gtgatggagt tggccactcc ctctctgcg gctcgctcg tctactgaggc 60

cgggcgacca aaggtcgccc gacgcccggg ctttgcccgg gcggcctcag tgagcgagcg 120
agcgcgcaga gagggagtgg ccaa 144

<210> 14
<211> 31
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(31)
<223> corresponds to base pairs 318-339 of AAV with an EcoR V site at the 5' end

<400> 14
gatatcgcca tgccgggggtt ttacgagatt g 31

<210> 15
<211> 35
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(35)
<223> corresponds to base pairs 1812 to 1846 of AAV

<220>
<221> mutation
<222> (20)..(20)

<220>
<221> mutation
<222> (23)..(23)

<400> 15
gcaccggttt gggctcactg atgtctgcgt cactg 35

<210> 16
<211> 35
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(35)
<223> corresponds to base pairs 1812 to 1846 of AAV

<220>
<221> mutation
<222> (13)..(13)

<220>
<221> mutation
<222> (16)..(16)

<400> 16
cagtgcgcga gacatcagtg agcccaaacg ggtgc 35

<210> 17
 <211> 29
 <212> DNA
 <213> adeno-associated virus

<220>
 <221> misc_feature
 <222> (1)..(29)
 <223> corresponds to base pairs 2261 to 2289 of AAV

<400> 17
 tgggccaggt ttgagcttcc accactgtc 29

<210> 18
 <211> 55
 <212> DNA
 <213> adeno-associated virus

<220>
 <221> misc_feature
 <222> (1)..(27)
 <223> corresponds to base pairs 2261-2289 of AAV

<220>
 <221> misc_feature
 <222> (28)..(53)
 <223> corresponds to base pairs 4330-4355 of AAV

<400> 18
 gacagtgggtg gaagctcaaa cctggcccaa gcacctgaat ggcacctatg attac 55

<210> 19
 <211> 28
 <212> DNA
 <213> adeno-associated virus

<220>
 <221> misc_feature
 <222> (1)..(28)
 <223> corresponds to base pairs 4446-4467 of AAV with a BamHI site at the 3' end

<400> 19
 ggatcccgca gagaccaaag ttcaactg 28

<210> 20
 <211> 27
 <212> DNA
 <213> adeno-associated virus

<220>
 <221> misc_feature
 <222> (1)..(27)
 <223> corresponds to base pairs 1852 to 1878, BamHI site at the 5' end

<400> 20
 agtcagttgc gcagccatcg acgtcag 27

<210> 21
 <211> 35

<212> DNA
 <213> adeno-associated virus

<220>
 <221> misc_feature
 <222> (1)..(35)
 <223> corresponds to base pairs 4302 to 4329, with a Not I site at the
 3' end

<400> 21
 gcggccgctt aacagacttg ttgtagttgg aagtg 35

<210> 22
 <211> 592
 <212> DNA
 <213> Homo sapiens

<400> 22
 gcgtgaagag ctgcagtgct actcttaaag ctgaattaat ctctgccatt ccttaaggaa 60
 acaggcaact gtcttaaaac cgtgggtttg aaaatatattt gttcaagata aaactgtttt 120
 aagatatatg tatatatatc ttatatatct gtattcgcat ggtaacatat cttcgggtctt 180
 cctgccgctg ggctctcagc ggccctccaa ggcagcccgc aggcccgtgc tcgcctcagg 240
 gatcctccac agccccgggg agaccttgcc tctaaagttg ctgcttttgc agctctgcca 300
 caaccgcgcg tcctcagagc cagccgggag gagctagaac cttccccgcg tttctttcag 360
 cagccctgag tcagaggcgg gctggccttg caagtagccg cccagccttc ttcggtctca 420
 cggaccgatc cggccgaacc ttctcccggg gtcagcgccg cgctgcgccg cccggctgac 480
 tcagcccggg cgggcgggcg ggaggctctc gactgggcgg gaagggtgcg gaagggtcgc 540
 ggcgggcggg tcggggaggt gcaaaaggat gaaaagcccg tggacggagc tg 592